guished by antibiograms using the Microscan method to determine elevated levels of ceftazidime, cefotaxime and aztreonam. Isolates were examined for the presence of a gene coding for the four CTX-M ESBL-enzyme groups by amplification with specific primers for the different groups and for the blaSHV SHV-gene specific primers. Bidirectional sequencing was done for genes amplified to determine strains differences.

Results: The 30 form 2006 gave ceftazidime and cefotaxime MIC ratios >16 and 32 mg/ml respectively, implying production of ESBLs. DNA amplification identified genes of the blaSHV type in the isolates from the neonates and both blaCTX-M1 and blaSHV types in the other isolates. The prevalences of CTX-M1-type, SHV-type and a dual carriage was 14%, 46% and 14% respectively. Sequencing further identified several subtypes including SHV-1, -2, -2a, 5, -5a -12, and -31 enzymes and three CTX-M1 types (CTX-3, -15 and -22). It is possible that the remaining isolates may have the blaTEM type gene that was not expected and therefore not tested.

Conclusion: The relatively high numbers of K. pneumoniae harbouring the CTX-M-type ESBLs enzymes in theBloemfontein hospital isolates is alarming and further investigations into the extent of the problem needs urgent attention.

doi:10.1016/j.ijid.2008.05.306

17.042

Genetic Diversity of Clinical and Zoonotic Multidrug-Resistant Salmonella in Malaysia

K.L. Thong1, a, B. Douadi1, W.L. Lai1, N. Ahmad2, R.M. Yasin3, S.D. Puthucheary1

1 University of Malaya, Kuala Lumpur, Malaysia
2 Institute for Medical Research, Kuala Lumpur, Malaysia

Background: Salmonella enterica serovars are among the most important agents of food-borne infections throughout the world. Serovars Typhimurium and Enteritidis are the most prevalent non-typhoidal Salmonella in Malaysia. Strains of Salmonella which are resistant to a range of antimicrobials, including first-choice agents for the treatment of humans, have emerged and are threatening to become a serious public health problem. The objectives of the study are to determine the rates of antimicrobial resistance and the genomic diversity of Salmonella Typhimurium and S. Enteritidis and S. Corvalis.

Methods: 151 strains of Salmonellae including 47 S Typhimurium (14 clinical and 33 zoonotic), 90 S Enteritidis (32 clinical and 59 zoonotic) and 13 S. Corvalis (clinical), were tested with 15 different antibiotic discs. PCR was applied to detect the resistance genes and PFGE was used to determine the genomic differentiation of the Salmonellae.

Results: Overall, 25% of strains were multi-drug resistant (resist to more than 3 antibiotics). Resistance towards cephalosporin antibiotics was also observed: 3% of the isolates were resistant to ceftriaxone and cefotaxime, 3% to cefuroxime, 18% to cephalothin. Resistant genes (blaTEM, strA, sul, aad and tet), have been found among the Salmonella strains and are thought to be responsible for the emergence of MDR strains. PFGE subtyped Typhimurium, Enteritidis and Corvalis into 39, 14 and 3 pulsotypes respectively.

Conclusion: An emergence of MDR Salmonella to 3rd generation of cephalosporin was observed and high heterogeneity was found among the serotypes of Typhimurium and Enteritidis.

doi:10.1016/j.ijid.2008.05.307

17.043

Antibiotic Resistance Patterns and Genotypes of Helicobacter pylori Isolated from Ethnically Different Dyspeptic Patients in Kuala Lumpur Malaysia

H. Salasawati, a, M. Ramelah

HUKM, Bandar Tun Razak, Malaysia

Background: Data on Helicobacter pylori antibiotic susceptibilities in Malaysia are limited, despite resistance being a key factor in treatment failure. The present study determine antibiotic resistance rates and evaluates vacA alleles, cagA and cagE status of Helicobacter pylori isolates from dyspeptic patients in Kuala Lumpur, Malaysia in three ethnic groups: Malays, Chinese and Indians.

Methods: All patients with cultured positive H. pylori were recruited prospectively. H. pylori isolates were sub cultured from biopsies of the gastric antrum obtained from patients who underwent endoscopy for dyspepsia at the Hospital UKM. Gastric antral biopsies were subcultured on blood agar plates which were then incubated under microaerophilic conditions at 37◦C for 5 days. H. pylori strains were identified by their colonial morphology, Gram stain appearance, oxidase and urease positivity. The susceptibilities of H. pylori isolates were determined by disc diffusion and epsilometer (E) tests on 188 H. pylori isolates. Deoxyribonucleic acid (DNA) was extracted from the H. pylori isolates using the commercially available kit. Polymerase chain reaction was carried out to determine the genotypes (vacA alleles, cagA and cagE).

Results: In vitro resistance rates was 24.5% for metronidazole. High-level-resistance was a feature of all (100%) of the metronidazole (MIC>256mg/L) resistant strains. All isolates were susceptible to amoxyccillin and clarithromycin. No associations between resistance and either the gender or ethnic group (Malays, Chinese and Indians) of the patients were detected. Resistant and susceptible isolates were genotypically diverse with respect to cagA, cagE and vacA type.

Conclusion: This study showed metronidazole-resistance rate was 24.5% for H. pylori with none of the isolates resistance to amoxyccillin and clarithromycin. Continued surveillance, particularly of high-level resistance of metronidazole (MIC>256mg/L), is recommended to monitor the effects of the treatment strategy for H. pylori eradication. Further study is required to correlate these findings with clinical response to antimicrobial therapy in patients with H. pylori infection.

doi:10.1016/j.ijid.2008.05.308